

SEP 10 2003

TECH CE



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/895,263A

DATE: 09/08/2003

TIME: 08:55:58

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\09082003\I895263A.raw

3 <110> APPLICANT: He, et al.  
 5 <120> TITLE OF INVENTION: Antibodies to Interleukin-1 Beta Converting Enzyme Like  
 \*Apoptosis

6       Protease 3  
 7       and 4

9 &lt;130&gt; FILE REFERENCE: PF140C2

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/895,263A

12 &lt;141&gt; CURRENT FILING DATE: 2001-07-02

14 &lt;150&gt; PRIOR APPLICATION NUMBER: 08/334,251

15 &lt;151&gt; PRIOR FILING DATE: 1994-11-01

17 &lt;160&gt; NUMBER OF SEQ ID NOS: 14

19 &lt;170&gt; SOFTWARE: PatentIn version 3.2

21 &lt;210&gt; SEQ ID NO: 1

22 &lt;211&gt; LENGTH: 1369

23 &lt;212&gt; TYPE: DNA

24 &lt;213&gt; ORGANISM: Homo sapiens

26 &lt;400&gt; SEQUENCE: 1

27	gcacgagaaa	ctttgcgtgt	cgcgttctcc	cgcgcgcggg	ctcaactttg	tagagcgagg	60
29	gccaacttg	gcagagcgcg	cggccagctt	tgcagagagc	gccctccagg	gactatgcgt	120
31	gccccggacac	gggtcgcttt	gggcttcc	acccttcgaa	agcgcactac	cccgagccag	180
33	ggcggtgca	agccccgc	ggcccttaccc	aggggggctc	ctccctccgc	agcgccgaga	240
35	cttttagttt	cgtttcgct	aaaggggccc	cagaccctt	ctgcggagcg	acggagagag	300
37	actgtgccag	tcccagccgc	cctaccgc	tggaaacgt	ggcagatgt	caggctgt	360
39	ttaaagagca	gggggtttag	gattcagcaa	atgaagattc	agtggatgt	aagccagacc	420
41	ggtcctcggt	tgtaccgtcc	cttttcgata	agaagaagaa	aatgttacc	atgcgtatcca	480
43	tcaagaccac	ccgggaccga	gtgccttacat	atcagtacaa	catgaaaa	aaaaagctgg	540
45	gcaaataatgc	cataataaac	aacaagaact	ttgataaaat	gacaggtat	ggcgatcgaa	600
47	acggaaacaga	caaagatgcc	gaggcgctt	tcaagtgtt	ccgaaggctt	ggttttgacg	660
49	tgtttgttata	taatgtactc	tcttgtcc	agatcaaga	tctgtttaaa	aaagcttctg	720
51	aaggaggacca	tacaatgtcc	gcctgttt	cctgcattt	cttaagccat	ggagaagaaa	780
53	atgttaattt	tggaaagat	gtgttcacac	caataaagga	tttgacagcc	cacttttaggg	840
55	ggatagatgt	caaaaaccctt	ttagagaaac	ccaaactt	cttcattt	gcttgcgcag	900
57	ggaccggact	tgtatgttgc	atccaggcc	actcggggcc	catcaatgtac	acagatgtca	960
59	atccctcgata	caagatccca	gttggaaagct	acttcctt	cgcctattcc	acggttccag	1020
61	gttattactc	gtggaggagc	ccaggaagag	gttcgtt	tgttgcac	ctctgttcc	1080
63	tccctggagga	gcacggaaaa	gacctggaaa	tcatgcagat	cctcaccagg	gtaatgaca	1140
65	gatgtgccag	gcactttgag	tctcgttct	atgaccacaa	cttccatgt	aagaagcaga	1200
67	tccctgtgt	ggtctccatg	ctcaccaagg	aactctactt	cagtcaatag	ccatatcagg	1260
69	ggtacattct	agctgagaag	caatgggtca	ctcattaatg	aatcacattt	ttttatgttc	1320
71	ttaaattt	cagaatttct	ccaggattt	aatttcagga	aaatgtatt		1369

74 &lt;210&gt; SEQ ID NO: 2

75 &lt;211&gt; LENGTH: 303

76 &lt;212&gt; TYPE: PRT

77 &lt;213&gt; ORGANISM: Homo sapiens

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79 <400> SEQUENCE: 2

81 Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser  
 82 1 5 10 15

85 Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val  
 86 20 25 30

89 Pro Ser Leu Phe Ser Lys Lys Lys Asn Val Thr Met Arg Ser Ile  
 90 35 40 45

93 Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe  
 94 50 55 60

97 Glu Lys Leu Gly Lys Cys Ile Ile Asn Asn Lys Asn Phe Asp Lys  
 98 65 70 75 80

101 Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala  
 102 85 90 95

105 Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn  
 106 100 105 110

109 Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu  
 110 115 120 125

113 Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His  
 114 130 135 140

117 Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys  
 118 145 150 155 160

121 Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu  
 122 165 170 175

125 Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp  
 126 180 185 190

129 Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn  
 130 195 200 205

133 Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser  
 134 210 215 220

137 Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp  
 138 225 230 235 240

141 Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu  
 142 245 250 255

145 Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His  
 146 260 265 270

149 Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile  
 150 275 280 285

153 Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln  
 154 290 295 300

157 <210> SEQ ID NO: 3

158 <211> LENGTH: 1159

159 <212> TYPE: DNA

160 <213> ORGANISM: Homo sapiens

162 <400> SEQUENCE: 3

163 gcacgagcgg atgggtgcta ttgtgaggcg gttgtagaag agtttcgtga gtgctcgca 60  
 165 ctcatacctg tggctgtgta tccgtggcca cagctggttg gcgtgcgcctt gaaatcccag 120  
 167 gccgtgagga gtagcgcgc cctgctcaca ctcggcgctc tggtttcgg tgggtgtgcc 180  
 169 ctgcacacctc ctcttccccgc attctcatata ataaaaggat ccatggagaa cactgaaaaac 240  
 171 tcagtggatt caaaaatccat taaaaatttg gaaccaaaga tcatacatgg aagcgaatca 300

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173	atggactctg	aatatccct	ggacaacagt	tataaaatgg	attatcctga	gatgggtta	360										
175	tgtataataa	ttaataataa	gaattttcat	aaaagcactg	aatgacatc	tcgtctgg	420										
177	acagatgtcg	atgcagcaaa	cctcaggaa	acattcagaa	acttcaaata	tgaagtca	480										
179	aataaaaatg	atcttacacg	tgaagaaatt	gtgaaattga	tgctgtatgt	ttctaaagaa	540										
181	gatcacagca	aaaggagcag	ttttgttgt	gtgcttctga	gccatggta	agaaggaata	600										
183	attttggaa	caaattggacc	tgttgacctg	aaaaaaataa	caaactttt	cagagggat	660										
185	cgtttagaa	gtctaactgg	aaaacccaaa	ctttcatta	ttcaggcctg	ccgtggtaca	720										
187	gaactggact	gtggcattga	gacagacagt	ggtgttcat	atgacatggc	gtgtcataaa	780										
189	ataccagtgg	aggccgactt	tttgtatgca	tactccacag	cacctggta	ttatttcttgg	840										
191	cggaaattcaa	aggatggctc	ctgggtcatc	cagtcgctt	gtgccatgt	gaaacagtat	900										
193	gcccacaagc	ttgaatttat	gcacatttt	accgggtta	accgaaaggt	ggcaacagaa	960										
195	ttttagtgcct	tttccttga	cgctacttt	catgaaaga	aacagattcc	atgtattgtt	1020										
197	tccatgctca	caaaaact	ctattttat	cactaaagaa	atggttggtt	gggggttttt	1080										
199	tttagttgt	atgccaagtg	agaagatggt	atattgggt	actgtatttc	cctctcattt	1140										
201	gggacctact	ctcatgctg					1159										
204	<210>	SEQ ID NO:	4														
205	<211>	LENGTH:	277														
206	<212>	TYPE:	PRT														
207	<213>	ORGANISM:	Homo sapiens														
209	<400>	SEQUENCE:	4														
211	Met	Glu	Asn	Thr	Glu	Asn	Ser	Val	Asp	Ser	Lys	Ser	Ile	Lys	Asn	Leu	
212	1				5				10						15		
215	Glu	Pro	Lys	Ile	Ile	His	Gly	Ser	Glu	Ser	Met	Asp	Ser	Gly	Ile	Ser	
216					20				25						30		
219	Leu	Asp	Asn	Ser	Tyr	Lys	Met	Asp	Tyr	Pro	Glu	Met	Gly	Leu	Cys	Ile	
220					35				40						45		
223	Ile	Ile	Asn	Asn	Lys	Asn	Phe	His	Lys	Ser	Thr	Gly	Met	Thr	Ser	Arg	
224					50				55						60		
227	Ser	Gly	Thr	Asp	Val	Asp	Ala	Ala	Asn	Leu	Arg	Glu	Thr	Phe	Arg	Asn	
228					65				70			75			80		
231	Leu	Lys	Tyr	Glu	Val	Arg	Asn	Lys	Asn	Asp	Leu	Thr	Arg	Glu	Glu	Ile	
232						85				90					95		
235	Val	Glu	Leu	Met	Arg	Asp	Val	Ser	Lys	Glu	Asp	His	Ser	Lys	Arg	Ser	
236						100				105					110		
239	Ser	Phe	Val	Cys	Val	Leu	Leu	Ser	His	Gly	Glu	Glu	Gly	Ile	Ile	Phe	
240						115				120					125		
243	Gly	Thr	Asn	Gly	Pro	Val	Asp	Leu	Lys	Lys	Ile	Thr	Asn	Phe	Phe	Arg	
244						130				135					140		
247	Gly	Asp	Arg	Cys	Arg	Ser	Leu	Thr	Gly	Lys	Pro	Lys	Leu	Phe	Ile	Ile	
248						145				150			155		160		
251	Gln	Ala	Cys	Arg	Gly	Thr	Glu	Leu	Asp	Cys	Gly	Ile	Glu	Thr	Asp	Ser	
252							165				170			175			
255	Gly	Val	Asp	Asp	Asp	Met	Ala	Cys	His	Lys	Ile	Pro	Val	Glu	Ala	Asp	
256							180				185			190			
259	Phe	Leu	Tyr	Ala	Tyr	Ser	Thr	Ala	Pro	Gly	Tyr	Tyr	Ser	Trp	Arg	Asn	
260							195				200			205			
263	Ser	Lys	Asp	Gly	Ser	Trp	Phe	Ile	Gln	Ser	Leu	Cys	Ala	Met	Leu	Lys	
264							210				215			220			
267	Gln	Tyr	Ala	Asp	Lys	Leu	Glu	Phe	Met	His	Ile	Leu	Thr	Arg	Val	Asn	

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268 225                230                235                240  
 271 Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
 272                245                250                255  
 275 His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu  
 276                260                265                270  
 279 Leu Tyr Phe Tyr His  
 280                275  
 283 <210> SEQ ID NO: 5  
 284 <211> LENGTH: 31  
 285 <212> TYPE: DNA  
 286 <213> ORGANISM: Artificial sequence  
 288 <220> FEATURE:  
 289 <223> OTHER INFORMATION: Contains a Bam HI restriction enzyme site (underlined)  
 followed  
 290                by 18 nucleotides of ICE-LAP-3 coding sequence starting from the  
 291                presumed terminal amino acid of the processed protein codon  
 293 <400> SEQUENCE: 5  
 294 gatcgatcc atgcgtgcgg ggacacgggt c                31  
 297 <210> SEQ ID NO: 6  
 298 <211> LENGTH: 31  
 299 <212> TYPE: DNA  
 300 <213> ORGANISM: Artificial sequence  
 302 <220> FEATURE:  
 303 <223> OTHER INFORMATION: Contains complementary sequences to an Xba I site followed  
 by 21  
 304                nucleotides of ICE-LAP-3  
 306 <400> SEQUENCE: 6  
 307 gtactctaga tcattcaccc tggtggagga t                31  
 310 <210> SEQ ID NO: 7  
 311 <211> LENGTH: 31  
 312 <212> TYPE: DNA  
 313 <213> ORGANISM: Artificial sequence  
 315 <220> FEATURE:  
 316 <223> OTHER INFORMATION: Contains a Bam HI restriction enzyme site followed by 18  
 317                nucleotides of ICE-LAP-4 coding sequence starting from the  
 318                presumed terminal amino acid of the processed protein codon  
 320 <400> SEQUENCE: 7  
 321 gatcgatcc atggagaaca ctgaaaactc a                31  
 324 <210> SEQ ID NO: 8  
 325 <211> LENGTH: 31  
 326 <212> TYPE: DNA  
 327 <213> ORGANISM: Artificial sequence  
 329 <220> FEATURE:  
 330 <223> OTHER INFORMATION: Contains complementary sequences to an Xba I site followed  
 by 21  
 331                nucleotides of ICE-LAP-4  
 333 <400> SEQUENCE: 8  
 334 gtactctaga tttagtgataa aaatagagtt c                31  
 337 <210> SEQ ID NO: 9  
 338 <211> LENGTH: 22  
 339 <212> TYPE: DNA  
 340 <213> ORGANISM: Artificial sequence

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342 <220> FEATURE:  
 343 <223> OTHER INFORMATION: Contains the ICE-LAP-3 translational initiation site ATG followed  
 344 by 5 nucleotides of ICE-LAP-3 coding sequence starting from the  
 345 initiation codon  
 347 <400> SEQUENCE: 9  
 348 gactatgcgt gcggggacac gg 22  
 351 <210> SEQ ID NO: 10  
 352 <211> LENGTH: 53  
 353 <212> TYPE: DNA  
 354 <213> ORGANISM: Artificial sequence  
 356 <220> FEATURE:  
 357 <223> OTHER INFORMATION: Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-3 coding sequence, not including the stop codon  
 359  
 361 <400> SEQUENCE: 10  
 362 aatcaagcgt agtctggac gtcgtatggg tattcaccct ggtggaggat ttg 53  
 365 <210> SEQ ID NO: 11  
 366 <211> LENGTH: 21  
 367 <212> TYPE: DNA  
 368 <213> ORGANISM: Artificial sequence  
 370 <220> FEATURE:  
 371 <223> OTHER INFORMATION: Contains the ICE-LAP-4 translational initiation site, ATG, followed by 15 nucleotides of ICE-LAP-4 coding sequence starting from the initiation codon  
 373  
 375 <400> SEQUENCE: 11  
 376 accatggaga acactgaaaa c 21  
 379 <210> SEQ ID NO: 12  
 380 <211> LENGTH: 53  
 381 <212> TYPE: DNA  
 382 <213> ORGANISM: Artificial sequence  
 384 <220> FEATURE:  
 385 <223> OTHER INFORMATION: Contains translation stop codon, HA tag and the last 21 nucleotides of the ICE-LAP-4 coding sequence, not including the stop codon  
 387  
 389 <400> SEQUENCE: 12  
 390 aatcaagcgt agtctggac gtcgtatggg tagtgataaa aatagagttc ttt 53  
 393 <210> SEQ ID NO: 13  
 394 <211> LENGTH: 503  
 395 <212> TYPE: PRT  
 396 <213> ORGANISM: Caenorhabditis elegans  
 398 <400> SEQUENCE: 13  
 400 Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met  
 401 1 5 10 15  
 404 Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala  
 405 20 25 30  
 408 Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly  
 409 35 40 45  
 412 Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg  
 413 50 55 60

**VERIFICATION SUMMARY**

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